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Sequence 461, App
Sequence 30160, A
Sequence 13421, A
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11424, A
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4317, Ap
33, Appl
5562, Ap
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4289, Ap
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9000, Ap
10152, A
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Sequence 15143, A
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Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-248-796A-15143
US-09-252-991A-3421
US-09-172-952-32
US-09-172-952-34
US-09-172-952-33
US-09-172-952-33
US-09-172-952-33
US-09-172-952-33
US-09-172-952-33
US-09-172-952-33
US-09-172-958-33
US-09-184-000C-6065
US-08-926-842B-21
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S-08-840-683-11

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S-09-926-842B-20

S-09-489-039A-8943

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-09-489-039A-12402
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-09-489-039A-13768
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US-09-248-796A-15143
Sequence 15143, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WOMBER: US/09/248,796A
TITLE OF INVENTION WOMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-09-13
PRIOR FILING DATE: 1998-09-13
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Sequence 43331, Application US/09270767
Sequence 43331, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
TITLE OF INVENTION:
NUCLEIC REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SEQ ID NO 43331
LENGTH: 240
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US-09-540-236-2717
US-09-129-112-15
US-08-081-929-10
US-09-489-039A-8023
US-09-911-842A-4
US-09-553-680-2
US-09-553-680-2
US-09-511-842A-7
US-09-181-030-7
US-09-514-671-7
US-09-182-113-7
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US-09-183-113-7
US-09-181-113-7
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US-09-270-767-43331
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Best Local Similarity 68.9
Matches 124; Conservative
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Sequence 13421, Application US/09489039A

Sequence 13421, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: PREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION UNDER: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30160
LENGTH: 238
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183 DTCAVIVRRHGIFVWGPTIDKAKIFNEAIDYLMELAIKMYQMGI-PPDCGIGE
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12.7%; Score 168.5; DB 4;
Best Local Similarity 25.7%; Pred. No. 2.3e-10;
Matches 54; Conservative 33; Mismatches 110;
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; Sequence 30160, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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US-09-252-991A-30160
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Matches 47; Conserv
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US-09-489-039A-13421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 CDINEKD-ISGPSPSKKLKKSQCTPLFMNAYTWRGAGAVIHTHSKAAVWATLLFPGREFK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 461, Application US/09538092
; Sequence 461, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Lolo:
APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same; TITLE OF INVENTION: WUMBER: US/09/538,092
; CURRENT APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatseqFormatter Version 0.9
; SEQ ID NO 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 LLFPG-REFKITHQEMIKGIKKCTSG-----GYYRYDDMLVVPIIENTPEEKGLKD 175
                                                                                                                                                                                                                                                                                                                       45 KDPNHPANLICELCRLFYDNNWVTGTGGGISIRDVDGPNPNLVYIAPSGVQKERIQPWEM 104
                                                                                                                                                                                                                                                                               19 ODKEHPRYLIPELCKOFYHLGWVTGTGGGISLKHGDE----IYIAPSGVQKERIQPEDM 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AQDKEHPRYLIPELCKQFYHLGWVTGTGGGISLK--HGDEIYIAPSGVQKERIQPEDMFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 RMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                       23;
                                                                                                                                                                                          Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.9%; Pred. No. 1.4e-46;
Matches 107; Conservative 37; Mismatches 69; Indels
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YJR024C
                                                                                                                                                                                       Query Match
41.3%; Score 546.5; DB 4
Best Local Similarity 50.4%; Pred. No. 3.3e-52;
Matches 118; Conservative 29; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Saccharomyces cerevisiae
                         NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15143
LENGTH: 284
                                                                                               TYPE: PRT
, ORGANISM: Candida albicans
US-09-248-796A-15143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; US-09-538-092-461
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Query Match 10.3%; Score 136; DB 4; Length 234; Best Local Similarity 30.2%; Pred. No. 9.2e-07; Matches 55; Conservative 22; Mismatches 73; Indels
 Length 238;
                                  78; Indels
 th 10.4%; Score 137; DB 3; Similarity 30.5%; Pred. No. 7.3e-07; 61; Conservative 21; Mismatches 78
                                                                                                                                                                                                                                                                     202 --ETWEKAKTMCEC-YDYLF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                   180 AADAVHNAVVLEECAYMGLF 199
Query Match
Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KA 207
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                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-583-110-4749
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                                     98 TPLFMNAYTM-RGAGAVIHTHSKAAVMATLLFPGREFKITHQEMIKGIKKCTSGGYYRYD 156
                                                                                  157 DMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWGETWEKAKTMCECYDY 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 ISGPSPSKKLKKSQCTPLFMNAYTMRG-AGAVIHTHSKAAVM---ATLLFPGREFKITHQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMIKGIKKCTS-----GGYYRYDDMLVVPIJENTPEEKGLKDRMAHAMNEYPDSCAVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 DYFYGAIPCTROMTAEEINGEYEYQ---TGEVIIETFEERG-----RSPAQIP---AVL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 LIPELCKOFYHLGWVTGTGGGISLKHGDE----IYIAPSGVQKERIOPEDMFVCDINEKD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 VHSHGPPAWGKNAADAVHNAVVLEECAYMGLFSRQLA-----PQLPAMQNELL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 VRRHGVYVWG----ETWEKAKTMCEC-YDYLFDIAVSMKKVGLDPSQLPVGENGIV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 145; DB 3; Length 231; 28.8%; Pred. No. 9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91; Indels
                                                                                                                                                                                                                                               US-09-172-952-32

Sequence 32, Application US/09172952

Patent No. 63681793

GENERAL INFORMATION:

APPLICANT: Hoch, James

APPLICANT: Dartoids, Veronique

TITLE OF INVENTION: METABOLIC SELECTION METHODS

FILE REFERENCE: 234/191

CURRENT APPLICATION NUMBER: US/09/172,952

CURRENT FILING DATE: 1998-10-14

NUMBER OF SEQ ID NOS: 33

SEQ ID NO 32

LENGTH: 231
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Fatent No. 6368793
GENERAL INFORMATION:
APPLICANT: HOCH, James
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILE REFERENCE: 234/191
CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 18
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.81
Matches 68; Conservative
                                                                                                                                                    217 LFDIAVSMKK 226
                                                                                                                                                                                 193 LFECELMRRR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: YiaS-EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: YiaS-Ko
US-09-172-952-18
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Sequence 4749, Application US/09583110

Sequence 4749, Application US/09583110

Barent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus;

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATHOD-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 4749
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US-09-107-532A-4317
; Sequence 4317. Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 DLPTHVQLYKAWSEIGSVVHTHSTEAV--GWAQAGRDIPFYGTTHADYFYGSIPCARSLT 135
                                                                                                                                                                                                                                            74 SSDTPTHLALYRRYPQIGGIVHTHSRHATIWSQAGLDLPA--WGTTHADYFYGAIPCTRR 131
                                                                                                                                                                                                                                                                                                                                                                                        132 MTVEEINGEYEYQ---TGEVIIKTFEQRGLDPA----QIP---AVLVHSHGPFAWGKD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 KDEVEVAYEKDTGLV--1VEEF-EHRGLNP-----VEVP---GIVVRNHGPFTWGKNPE 183
                                                                                                                                                                                                                                                                                                                                             150 -----GGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCAVLVRRHGVYVWG-- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 CTPLFMNAY-TMRGAGAVIHTHSKAAVMATLLFPGRE---FKITHQEMIKGIKKCTSG-- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GLVKFTWGNVSEVNRELGVIVIKPSGVDYDELTPENMVVTDLDGKILEG-----DLRPSS 77
                                                                                                                                 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GWYTGTGGGISLKHGD--EIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKSQ 96
                                                                                                                                 20 GLVTFTWGNVSAV--DETRKLMVIKPSGVEYEVMTADDMVVVEM----ASGKVVEGGKKP
                                                                                                                                                                                                        95 SQCTPLFMNAY-TMRGAGAVIHTHSKAAVM---ATLLFPGREFKITHQEMIKGIKKCTS-
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                                                                    39 GWVTGTGGGTSLKHGDE----IYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKK
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40;
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Gaps

33;

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Sequence 5562, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 KSQCTPLFWNAY-TWRGAGAVIHTHSK-AAVMATLLFPGREFKITHQEMIKGIKKCT--- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 ----SGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSC-AVLVRRHGVYVWGE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PDNIPAVLVHSHGPFAWGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 YHLGWVTGTGGGISL--KHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| || || : : : || || || : : || || || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 || 19 |
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.8%; Score 129.5; DB 3; Length 231; Best Local Similarity 27.8%; Pred. No. 4.7e-06; Matches 50; Conservative 24; Mismatches 73; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMEUTER: PC
COMEUTER: PC
CORRENT ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: UNABER: GIC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 TTKEIKGNY----ELETGKVIVETFLSRGIE-
                                     CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SEQ TWARE: TESTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 231
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 233 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5562: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7310
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
FILE REFERENCE: 234/191
                                                                                                                                                                                                                                                                                                                      ORGANISM: YiaS-Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-107-532A-5562
                                                                                                                                                                                                                                                                                                                                                            US-09-172-952-33
                                                                                                                                                                                                                                                                                     TYPE: PRT
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ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 DISGPSPSKKLKKSQCTPLFMNAY-TMRGAGAVIHTHSKAAVMATLLFPGRE---FKITH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 QEMIKGIKKCT------SGGYYRYDDMLVVPIJENTPEEKGLKDRMAHAMN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 ADAFYGKVPCTRQLTKEEVREAYEVHTGN-------VIVETFKERKLDP-----N 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 PRYLIPELCKOFYHLGWVTGTGGGISL--KHGDEIYIAPSGVQKERIQPEDMFVCDINEK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 PRY------GLVKLTWGNVSEVDRELGVIVIKPSGVRYECMQADQMVVTDLSGN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KTMCECYDYLFD 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                               ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-172-952-33
Sequence 31, Application US/09172952
Patent No. 6368793
GENERAL INFORMATION:
APPLICANT: Hoch, James
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...241
SEQUENCE DESCRIPTION: SEQ ID NO: 4317:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 EYPDSCAVLVRRHGVYVWGETWEKA----
                                                                                                                                                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                         STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 241 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4317: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   STATE: Massachusetts
                                     NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
                                                                                                                                                                                                  CITY: Waltham
                                                                                                                                                                                                                                                                                 COUNTRY: USA
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GRUERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pheumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOD-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT PILING DATE: 1200-05-26
PRIOR PILING DATE: 1098-06-30
PRIOR PILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
NUMBER OF SEQ ID NOS: 5322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6065, Application US/09134000C
Batent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BATEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 EFKITHQEMIKGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEY-PDSCAV 190
                                                                                                                                                                                                         132 EFKITHQEMIKGIKKCTSGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEY-PDSCAV 190
                                                                                                                                                                                                                                           77 DINEKDISGPS---PSKKLKKSQCTPLFMNAYTMR-GAGAVIHTHSKAAV-MATLLFPGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 NIKGEILEAEGDYCPSSEIK-----MHIRCYEEREDVRSVVHAHPPIATGFALAHIPLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 TYSLIESAIVVGAIPITPFG------VPSTMEVPE-----AITPYLPDHDVM 156
                                                                                                                 DINEKDISGPS---PSKKLKKSQCTPLFMNAYTMR-GAGAVIHTHSKAAV-MATLLFPGR 131
                            AODKEHPRYLIPELCKOFYHLGWVTGTGGGISLK-HGDBIYIAPSGVQKERIQPEDMFVC 76
                                                 2 SQDEKLIREQICDVCHKMWQLGWVAANDGNVSVRLDEDTILATPTGISKSFITPEKLVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AQDKEHPRYLIPELCKQFYHLGWVTGTGGGISLK-HGDEIYIAPSGVQKERIQPEDMFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
9.5%; Score 126; DB 4; Length 242;
Best Local Similarity 23.6%; Pred. No. 1.2e-05;
Matches 45; Conservative 30; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4289, Application US/09583110
Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                              157 LLENHGALTVG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 LVRRHGVYVWG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 LLENHGALTVG 167
                                                                                                                                                                                                                                                                                                    LVRRHGVYVWG
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US-09-134-000C-6065
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-583-110-4289
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                   78 INEKDISGPSPSKKLKKSQCTPLFMNAY-TMRGAGAVIHTHSKAAVM---ATLLFPGREF 133
                                                                                                                                                                                                                                                                                                                                                                                                              134 KITHQEMIKGIKKCT----SGGYYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEY 184
                                                                                                                                                                                                                                 27 LIPELCKQFYHL-----GWVTGTGGGISLKHGDEIY--IAPSGVQKERIQPEDMFVCD 77
                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 PDSCAVLVRRHGVYVWGETWEKAKTMCECYDYLFDIAVSMKKVGLDPSQLP 235
                                                                                                                                                                                      43;
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                                                                                                                                            Length 233;
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                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCORNATION:
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
TITLE OF INVENTION: HEAT SHOCK PROTEIN HSP72 FROM
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: ADDRESSES:
ADDRESSES: 1251 Avenue of the Americas
CITY: New York
STARE: New York
CUNTRY: United States of America
ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10020

ZIP: 10020

MEDIUM TYPER PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PROPERTING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,534
                                                                                                                                    Query Match 9.6%; Score 127.5; DB 4; Best Local Similarity 26.8%; Pred. No. 8e-06; Matches 62; Conservative 29; Mismatches 97;
;
LOCATION: (B) LOCATION 1...233
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5562:
US-09-107-532A-5562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F
REGISTRATION NUMBER: 27,794
REFRENCE/DOCKET NUMBER: Blove
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-900
TELEX: 14-9367
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08472534
Patent No. 5919620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 242 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 LGLVKLTWGNVSEINRSLGIIVIKPSGVKYQEMTKEQMVVTDLKGQLLE----TNALKPS 84
                                                                                                                                                                                                                                                                                                                                                                             38 LGWVTGTGGGIS--LKHGDEIYIAPSGVQKERIQPEDMFVCDINEKDISGPSPSKKLKKS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 -----LSESEIKENYEEFTG-KVIVETFHEQELDPLAVPGVLVYGHGPFTWGMTPEKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 YYRYDDMLVVPIIENTPEEKGLKDRMAHAMNEYPDSCA----ULVRRHGVYVWGETWEKA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/08926842B
Patent No. 6030807
CENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              81; Indels 23; Gaps
                                                                                                                                                                                                                                                                           Query Match 9.5%; Score 125.5; DB 4; Length 241; Best Local Similarity 31.8%; Pred. No. 1.4e-05; Matches 57; Conservative 18; Mismatches 81; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/926,842B

FILING DATE: 10-SEP-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERNICE/DOCKET NUMBER: 600-1-089 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SSOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 6065
LENGTH: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                              TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 240 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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HYPOTHETICAL:
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